SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Pulst, Stefan M.

(ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Pretty, Schroeder & Poplawski
- (B) STREET: 444 South Flower Street, Suite 2000
- (C) CITY: Los Angeles
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 90071

(v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" diskette
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/727,084
- (B) FILING DATE: October 8, 1996
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Viviana Amzel, Ph. D.
- (B) REGISTRATION NUMBER: 30930
- (C) REFERENCE/DOCKET NUMBER: P07 37217

(ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 213-622-7700
- (B) TELEFAX: 213-489-4210

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCGG CTCCCGGCGG CTCCTTGGTC 60

TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC 120

CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TGCGTCCCCG CCGCGTTCCG 180

GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG 240

GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300

AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360

AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT 420

CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480

GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC 516

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG 60

GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG 120

CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG 174
Met Arg Ser Ala
1

GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC 222
Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe
5 10 15 20

GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG 270
Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg
25 30 35

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CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC        318
Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser
             40                  45                  50

GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC        366
Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser
         55                  60                  65

TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC        414
Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly
     70                  75                  80

GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT        462
Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro
 85                  90                  95                  100

CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC        510
Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala
                105                 110                 115

CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC        558
Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser
            120                 125                 130

CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC        606
Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro
        135                 140                 145

CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG        654
Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys
    150                 155                 160

CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG        702
Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
165                 170                 175                 180

CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC        750
Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg
                185                 190                 195

AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG        798
Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser
            200                 205                 210

CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG        846
Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser
        215                 220                 225

GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT        894
Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly
    230                 235                 240

CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA        942
Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly
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245                 250                 255                 260

ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC      990
Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly
                265                 270                 275

TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT     1038
Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val
            280                 285                 290

TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT     1086
Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His
        295                 300                 305

GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG     1134
Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met
    310                 315                 320

GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA     1182
Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys
325                 330                 335                 340

GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT     1230
Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala
                345                 350                 355

ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC     1278
Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro
            360                 365                 370

TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA     1326
Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu
        375                 380                 385

AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT     1374
Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn
    390                 395                 400

GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG     1422
Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser
405                 410                 415                 420

TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG     1470
Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg
                425                 430                 435

GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG     1518
Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln
            440                 445                 450

TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA     1566
Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu
        455                 460                 465
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AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC      1614
Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser
    470                 475                 480

ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA      1662
Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
485                 490                 495                 500

GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC      1710
Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly
                505                 510                 515

CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA      1758
Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser
            520                 525                 530

GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT      1806
Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly
        535                 540                 545

GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT      1854
Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser
    550                 555                 560

CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT      1902
Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro
565                 570                 575                 580

ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT      1950
Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser
                585                 590                 595

CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA      1998
His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys
            600                 605                 610

CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA      2046
Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg
        615                 620                 625

CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT      2094
His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser
    630                 635                 640

GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT      2142
Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro
645                 650                 655                 660

CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA GTG GTC      2190
Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser Val Val
                665                 670                 675

AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC      2238
Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro
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            680                 685                 690

AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT      2286
Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser
        695                 700                 705

CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA      2334
Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro
    710                 715                 720

GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC      2382
Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr
725                 730                 735                 740

CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC      2430
Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn
                745                 750                 755

TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT      2478
Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro
        760                 765                 770

AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA      2526
Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu
        775                 780                 785

CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG      2574
His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg
    790                 795                 800

TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA      2622
Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys
805                 810                 815                 820

AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA      2670
Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu
                825                 830                 835

CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC      2718
Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn Cys Thr
            840                 845                 850

AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT      2766
Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu
        855                 860                 865

AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT      2814
Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val
    870                 875                 880

CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG      2862
Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu
885                 890                 895                 900
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AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT      2910
Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn
                905                 910                 915

GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT      2958
Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr
            920                 925                 930

ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT ATG GTG      3006
Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val
        935                 940                 945

GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT TTT GCA      3054
Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys Phe Ala
    950                 955                 960

CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA CCT TTA      3102
Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu
965                 970                 975                 980

TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG ACA TAT      3150
Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr
                985                 990                 995

AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT CAT CAG      3198
Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His His Gln
            1000                1005                1010

AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT GCA GCC      3246
Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile Ala Ala
        1015                1020                1025

ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG      3294
Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln
    1030                1035                1040

TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG      3342
Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln
1045                1050                1055                1060

CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG      3390
His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met
                1065                1070                1075

GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT      3438
Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ser Ala Thr
            1080                1085                1090

CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA      3486
Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys
        1095                1100                1105

TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC      3534
Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser
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    1110                1115                1120

ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC      3582
Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His
1125                1130                1135                1140

CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG      3630
Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln
                1145                1150                1155

CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC      3678
Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His
            1160                1165                1170

CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG      3726
His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln
        1175                1180                1185

CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG      3774
Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met
    1190                1195                1200

ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA      3822
Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala
1205                1210                1215                1220

CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT      3870
Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr
                1225                1230                1235

ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA      3918
Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser
            1240                1245                1250

GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG      3966
Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met
        1255                1260                1265

ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA      4014
Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala
    1270                1275                1280

CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG      4062
Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr
1285                1290                1295                1300

CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAAGGCTGCC           4108
His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
                1305                1310

CTGGAGGAAC CGAAAGGCCA AATTCCCTCC TCCCTTCTAC TGCTTCTACC AACTGGAAGC    4168

ACAGAAAACT AGAATTTCAT TTATTTTGTT TTTAAAATAT ATATGTTGAT TTCTTGTAAC    4228
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ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGGAAGAT ACTTGGACCG AGTAGAGGCA 4288

TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC CGCAGGTACC 4348

CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTTTA ATAACCCTTG AAAGTCATGA 4408

ACACATCAGC TAGCAAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC TGCTAAAAAA 4468

AAAAAAAAAA AAA 4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu
  1               5                  10                  15

Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln
             20                  25                  30

Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly
         35                  40                  45

Pro Tyr Pro Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro
     50                  55                  60

Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn
 65                  70                  75                  80

Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly
                 85                  90                  95

Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala
            100                 105                 110

Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly
        115                 120                 125

Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala
    130                 135                 140

Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr
145                 150                 155                 160

Met Ser Leu Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
                165                 170                 175
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Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala
            180                 185                 190

Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala
        195                 200                 205

Ala Ala Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr
    210                 215                 220

Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly
225                 230                 235                 240

Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile
                245                 250                 255

Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr
            260                 265                 270

Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile
        275                 280                 285

Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu
    290                 295                 300

Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg
305                 310                 315                 320

Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val
                325                 330                 335

Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe
            340                 345                 350

Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys
        355                 360                 365

Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu
    370                 375                 380

Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met
385                 390                 395                 400

Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser
                405                 410                 415

Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu
            420                 425                 430

Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu
        435                 440                 445

Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg
    450                 455                 460
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Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg
465 470 475 480

Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly
485 490 495

Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser
500 505 510

Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr
515 520 525

Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val
530 535 540

Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser
545 550 555 560

Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg
565 570 575

Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser
580 585 590

Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser
595 600 605

Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro
610 615 620

Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly
625 630 635 640

Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu
645 650 655

Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp
660 665 670

Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg
675 680 685

Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro
690 695 700

Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala
705 710 715 720

Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn
725 730 735

Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp
740 745 750

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Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn
        755                 760                 765

Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro
    770                 775                 780

Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys
785                 790                 795                 800

Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln
                805                 810                 815


Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys
            820                 825                 830

Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser
        835                 840                 845

Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser
    850                 855                 860

Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr
865                 870                 875                 880

Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp
                885                 890                 895

Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr
            900                 905                 910

Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro
        915                 920                 925

Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser
    930                 935                 940

Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro
945                 950                 955                 960

Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly
                965                 970                 975

Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln
            980                 985                 990

Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp
        995                 1000                1005

Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro
    1010                1015                1020

Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
1025                1030                1035                1040
```

Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
1045 1050 1055

Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
1060 1065 1070

Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser
1075 1080 1085

Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr
1090 1095 1100

Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
1105 1110 1115 1120

Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
1125 1130 1135

Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
1140 1145 1150

Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
1155 1160 1165

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
1170 1175 1180

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
1185 1190 1195 1200

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser
1205 1210 1215

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
1220 1225 1230

Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala
1235 1240 1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
1250 1255 1260

Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu
1265 1270 1275 1280

Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe
1285 1290 1295

Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..1255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
G CAC GAG GGG CCG CTC ACC ATG TCG CTG AAG CCG CAG CCG CAG CCG          46
  His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro
    1               5                  10                  15

CCC GCG CCC GCC ACT GGC CGC AAG CCC GGC GGC GGC CTG CTC TCG TCG        94
Pro Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser
                20                  25                  30

CCC GGC GCC GCG CCG GCC TCG GCC GCG GTG ACC TCG GCT TCC GTG GTG       142
Pro Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val
            35                  40                  45

CCG GCC CCG GCC GCG CCG GTG GCG TCT TCC TCG GCG GCC GCG GGC GGC       190
Pro Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly
        50                  55                  60

GGG CGT CCC GGC CTG GGC AGA GGT CGG AAC AGT AGC AAA GGA CTG CCT       238

Gly Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro
    65                  70                  75

CAG CCT ACG ATT TCT TTT GAT GGA ATC TAT GCA AAC GTG AGG ATG GTT       286
Gln Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val
80                  85                  90                  95

CAT ATA CTT ACG TCA GTT GTT GGA TCG AAA TGT GAA GTA CAA GTG AAA       334
His Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys
                100                 105                 110

AAC GGA GGC ATA TAT GAA GGA GTT TTT AAA ACA TAC AGT CCT AAG TGT       382
Asn Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys
            115                 120                 125

GAC TTG GTA CTT GAT GCT GCA CAT GAG AAA AGT ACA GAA TCC AGT TCG       430
Asp Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser
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        130                 135                 140

GGG CCA AAA CGT GAA GAA ATA ATG GAG AGT GTT TTG TTC AAA TGC TCA      478
Gly Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser
    145                 150                 155

GAC TTC GTT GTG GTA CAG TTT AAA GAT ACA GAC TCC AGT TAT GCA CGG      526
Asp Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg
160                 165                 170                 175

AGA GAT GCT TTT ACT GAC TCT GCT CTC AGC GCA AAG GTG AAT GGT GAG      574
Arg Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu
                180                 185                 190

CAC AAG GAG AAG GAC CTG GAG CCC TGG GAT GCA GGG GAG CTC ACG GCC      622
His Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala
            195                 200                 205

AGC GAG GAG CTG GAG CTG GAG AAT GAT GTG TCT AAT GGA TGG GAC CCC      670
Ser Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro
        210                 215                 220

AAT GAC ATG TTT CGA TAT AAT GAA GAG AAT TAT GGT GTG GTG TCC ACA      718
Asn Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr
    225                 230                 235

TAT GAT AGC AGT TTA TCT TCA TAT ACG GTT CCT TTA GAA AGG GAC AAC      766
Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn
240                 245                 250                 255

TCA GAA GAA TTT CTT AAA CGG GAG GCA AGG GCA AAC CAG TTA GCA GAA      814
Ser Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu
                260                 265                 270

GAA ATT GAA TCC AGT GCT CAG TAC AAA GCT CGT GTC GCC CTT GAG AAT      862
Glu Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn
            275                 280                 285

GAT GAC CGG AGT GAG GAA GAA AAA TAC ACA GCA GTC CAG AGA AAC TGC      910
Asp Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys
        290                 295                 300

AGT GAC CGG GAG GGG CAT GGC CCC AAC ACT AGG GAC AAT AAA TAT ATT      958
Ser Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile
    305                 310                 315

CCT CCT GGA CAA AGA AAC AGA GAA GTC CTA TCC TGG GGA AGT GGG AGA     1006
Pro Pro Gly Gln Arg Asn Arg Glu Val Leu Ser Trp Gly Ser Gly Arg
320                 325                 330                 335

CAG AGC TCA CCA CGG ATG GGC CAG CCT GGG CCA GGC TCC ATG CCG TCA     1054
Gln Ser Ser Pro Arg Met Gly Gln Pro Gly Pro Gly Ser Met Pro Ser
                340                 345                 350
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AGA GCT GCT TCT CAC ACT TCA GAT TTC AAC CCG AAC GCT GGC TCA GAC      1102
Arg Ala Ala Ser His Thr Ser Asp Phe Asn Pro Asn Ala Gly Ser Asp
            355                 360                 365

CAA AGA GTA GTT AAT GGA GGT GTT CCC TGG CCA TCG CCT TGC CCA TCT      1150
Gln Arg Val Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser
        370                 375                 380

CCT TCC TCT CGC CCA CCT TCT CGC TAC CAG TCA GGT CCC AAC TCT CTT      1198
Pro Ser Ser Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu
    385                 390                 395

CCA CCT CGG GCA GCC ACC CCT ACA CGG CCT CGT GCC GAA TTC CTG CAG      1246
Pro Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln
400                 405                 410                 415

CCC GGG GAT CC                                                      1257
Pro Gly Asp
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro Pro
 1               5                  10                  15

Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro
            20                  25                  30

Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val Pro
        35                  40                  45

Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly
    50                  55                  60

Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln
65                  70                  75                  80

Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val His
                85                  90                  95

Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn
            100                 105                 110

Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp
```

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        115                 120                 125

Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly
    130                 135                 140

Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser Asp
145                 150                 155                 160


Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg
                165                 170                 175

Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu His
            180                 185                 190

Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser
        195                 200                 205

Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn
    210                 215                 220

Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr
225                 230                 235                 240

Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser
                245                 250                 255

Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu
            260                 265                 270

Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp
        275                 280                 285

Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser
    290                 295                 300

Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro
305                 310                 315                 320

Pro Gly Gln Arg Asn Arg Glu Val Leu Ser Trp Gly Ser Gly Arg Gln
                325                 330                 335

Ser Ser Pro Arg Met Gly Gln Pro Gly Pro Gly Ser Met Pro Ser Arg
            340                 345                 350

Ala Ala Ser His Thr Ser Asp Phe Asn Pro Asn Ala Gly Ser Asp Gln
        355                 360                 365

Arg Val Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro
    370                 375                 380

Ser Ser Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro
385                 390                 395                 400
```

Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln Pro
405 410 415

Gly Asp